

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run On: January 16, 2003, 16:39:12 : Search time 7.28571 seconds
(without alignments)
28 464 Million cell updates/sec

Title: US-09-856-070-26
Perfect score: 28
Sequence: 1 QDYEE 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2600000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution

SUMMARIES

Result No.	Score	Query Match	Length	DE ID	Description
1	28	100.0	252	1 QDYEE_HUMAN	Q9Y566 homo sapien
2	28	100.0	262	1 QDYEE_MOUSE	Q9W618 mus musculus
3	28	100.0	338	1 PAHX_HUMAN	G14832 homo sapien
4	28	100.0	385	1 SWY_DYAR	Q9Y711 pyrodictus
5	28	100.0	505	1 SYE_CHLEP	Q92723 chlamydia p
6	28	100.0	540	1 ERI_HUMAN	P16776 bos taurus
7	28	100.0	585	1 ERI_HUMAN	P15311 homo sapien
8	28	100.0	624	1 DSK1_CYLFU	Q19493 cylinthrele
9	28	100.0	811	1 SWO_SCUBO	Q97278 schistosom
10	28	100.0	824	1 DQ20_HUMAN	Q9U816 homo sapien
11	28	100.0	875	1 E22_MOUSE	267314 mus musculi
12	28	100.0	1332	1 KAP_HUMAN	Q95163 homo sapien
13	25	89.3	82	1 Y070_METJA	Q60373 metanococc
14	25	89.3	130	1 CAL2_MOUSE	Q99893 mus muscult
15	25	89.3	134	1 CAL2_RAT	P18093 rattus norv
16	25	89.3	141	1 V336_HATIN	P42330 haemophilus
17	25	89.3	168	1 RIP3_TOBAC	Q03683 nicotiana t
18	25	89.3	187	1 EEP_MYCLE	Q9C850 mycobacteri
19	25	89.3	187	1 EEP_MYCTU	P95019 mycobacteri
20	25	89.3	203	1 DCC_DROME	P24156 drosophila
21	25	89.3	212	1 LIPB_HATIN	P44464 haemophilus
22	25	89.3	239	1 PHB3_ANEPH	P33632 anemia phyl
23	25	89.3	258	1 L231_HUMAN	Q75822 homo sapien
24	25	89.3	263	1 Y225_METJA	Q57678 metanococc
25	25	89.3	280	1 FEY2_DROME	P42280 drosophila
26	25	89.3	289	1 GWFN_SCHPO	Q9P776 schizosacch
27	25	89.3	290	1 RIP1_TOBAC	Q03681 nicotiana t
28	25	89.3	292	1 RIP2_TOBAC	Q03682 nicotiana t
29	25	89.3	293	1 RIP8_TOBAC	Q03686 nicotiana t
30	25	89.3	298	1 CTF_HUMAN	P20774 homo sapien
31	25	89.3	299	1 G1F_BOVIN	P19879 bos taurus
32	25	89.3	315	1 G4W_YEAST	P50085 saccharomye
33	25	89.3	339	1 V021_YEAST	P53352 saccharomye

RESULT 1

ORC6_HUMAN
ID ORC6_HUMAN STANDARD: PRT: 252 AA.
AC Q9V5N6;
DT 16-OCT-2001 (Rel. 40, Created)
DI 16-OCT-2001 (Rel. 40, Last sequence update)
DI 16-OCT-2001 (Rel. 40, Last annotation update)
DE Origin recognition complex subunit 6.
GN ORC6L.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_taxonomy:9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Dean F.B., O'Donnell M.;
RT "RNA cloned of a homolog for Saccharomyces cerevisiae gene from Homo sapiens."
RL Submitted (MAP-1999) to the EMBL/Genbank/Trna databases.
CC 1- FUNCTION: COMPONENT OF THE ORIGIN RECOGNITION COMPLEX (ORC) THAT BINDS ORIGINS OF REPLICATION. IT HAS A ROLE IN BOTH CHROMOSOMAL REPLICATION AND MATING TYPE TRANSCRIPTIONAL SILENCING. BINDS TO THE APS CONSENSUS SEQUENCE (ACS) OF ORIGINS OF REPLICATION IN AN ATP-DEPENDENT MANNER.
CC 2- SUBUNIT: ORC IS COMPOSED OF SIX SUBUNITS.
CC 3- SUBCELLULAR LOCATION: Nucleolus.
CC 4- SIMILARITY: BELONGS TO THE ORC6 FAMILY.
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DR EMBL: AF139658; AAC12666.1; -.
DR Genbank: HGNC:17151; ORC6L.
KW DNA replication; Nucleolus; Protein; DNA-binding;
SQ SEQUENCE 252 AA. 28.0% ID, 7884000-7051451E ORC6L;
Query Match: 100.0%; Score 28, FB 1, Length 252;
Best Local Similarity: 100.0%, Pred. No. 35;
Matches: 5, Conservative: 0, Mismatches: 0, Indels: 0, Gaps: 0;

QY

QY 1 QDYEE 5
DE 230 QDYEE 234
RESULT 2
ORC6_MOUSE
ID ORC6_MOUSE STANDARD: PRT: 252 AA.
AC Q9W0J8;
DI 16 OCT-2001 (Rel. 40, Created)
DI 16 OCT-2001 (Rel. 40, Last sequence update)

15-JUN-2002 (Ref. 41, Last annotation update)
 DE origin-recognition complex subunit 6.
 GN ORC6L OR ORC6
 OS Mus musculus (Mouse)
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 DX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Dean P.B., O'Donnell M.;
 RI "cDNA cloning of a homolog for Saccharomyces cerevisiae ORC6 from Mus
 RT musculus";
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBI databases
 CC -1- FUNCTION: COMPONENT OF THE ORIGIN RECOGNITION COMPLEX (ORC) THAT
 CC BINDS ORIGINS OF REPLICATION. IT HAS A ROLE IN BOTH CHROMOSOMAL
 CC REPLICATION AND MATING TYPE TRANSCRIPTIONAL SILENCING. BINDS TO
 CC THE ARS CONSENSUS SEQUENCE (ACS) OF ORIGINS OF REPLICATION IN AN
 CC ATP DEPENDENT MANNER (BY SIMILARITY).
 CC -1- SUBUNIT: ORC IS COMPOSED OF SIX SUBUNITS (BY SIMILARITY)
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE ORC6 FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AF159659; AAD32667.1;
 CC GDB: MGI:1929285; orc6l.
 CC DNA replication; Nuclear protein; DNA-binding.
 KW SEQUENCE: 262 AA; 29188 MW; F8027D39C87B16C CRC64.
 Query Match: 100.0%; Score 28; DB 1; Length 262;
 Best Local Similarity 100.0%; Pred. No. 36;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QDYEE 5
 DB 240 QDYEE 244
 |||||

 RESULT 1
 PAHX HUMAN
 ID PAHX HUMAN STANDARD; PPT: 338 AA.
 AF 0148432;
 DT 15-JUL-1999 (Ref. 48, Created)
 DT 15-JUL-1999 (Ref. 48, Last sequence update)
 DI 15-JUN-2002 (Ref. 41, Last annotation update)
 DE Phytanoyl-CoA dioxygenase, peroxisomal precursor (pPC) (phytanic acid oxidase).
 DE (Phytanoyl-CoA alpha-hydroxylase) (pHx) (phytanic acid oxidase).
 GN PHX1 OR PAHX.
 OS Homo sapiens (Human)
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 DX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND VARIANT REFSUM TRP-275.
 RA MEDLINE-97467740; PubMed-9326939;
 RA Mahalik S.J., Morrell J.C., Kim D., Sachsteder K.A., Watkins P.A.,
 RA Gould S.J.;
 RI "Identification of PAHX, a Refsum disease gene";
 RL Nat. Genet. 17:185-189(1997).
 CC [2]
 RP SEQUENCE FROM N.A. AND VARIANT REFSUM HIS-269
 RA MEDLINE-97467741; PubMed-9426940;
 RA Jansen G.A., Orman K., Ferdinandusse S., Bjlst L., Muijsers A.O.,
 RA Skjeldal O.H., Stokke O., Jakobs C., Wraith J.E.,
 RA Wanders K.J.A.;
 RI "Refsum disease is caused by mutations in the phytanoyl-CoA
 RT hydroxylase gene.";

Nat. Genet. 17:190-193(1997).
 [3]
 RP SEQUENCE FROM N.A.
 CC TISSUE-Leukemia;
 CC MEDLINE-95162545; PubMed-10051602;
 RA Chambraud B., Radanyi C., Camonis J.H., Rajkowski K., Schumacher M.,
 RA Baulieu E.-E.;
 RI "Immunophilins, refsum disease, and lupus nephritis: the peroxisomal
 RT enzyme phytanoyl-CoA alpha-hydroxylase is a new FKBP-associated
 RT protein.";
 RL Proc. Natl. Acad. Sci. U.S.A. 96:2104-2109(1999).
 RN [4]
 RP SEQUENCE FROM N.A., AND VARIANT REFSUM ALA-192 INS.
 RA PubMed-10767344;
 RA Jansen G.A., Hogenhout E.M., Ferdinandusse S., Waterham H.K.,
 RA Orman K., Jakobs C., Skjeldal O.H., Wanders K.J.A.;
 RI "Human phytanoyl-CoA hydroxylase: resolution of the gene structure and
 RT the molecular basis of Refsum's disease.";
 PL Hum. Mol. Genet. 9:1195-1200(2000).
 CC -1- FUNCTION: CONVERTS PHYTANOL-COA TO 2-HYDROXYPHYTANOL-COA.
 CC -1- CATALYTIC ACTIVITY: Phytanoyl-CoA + 2-oxoglutarate + O(2) -> 2-
 CC hydroxyphytanoyl-CoA + succinate + CO(2).
 CC -1- COFACTOR: Iron and ascorbate.
 CC -1- PATHWAY: Alpha-oxidation of 3-methyl branched fatty acids
 CC (phytanic acid); second step.
 CC -1- SUBUNIT: INTERACTS SPECIFICALLY WITH THE IMMUNOPHILIN FKBP52.
 CC -1- SUBCELLULAR LOCATION: Peroxisomal.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN LIVER, KIDNEY, AND T-CELLS, BUT
 CC NOT IN SPLEEN, BRAIN, HEART, LUNG, AND SKELETAL MUSCLE.
 CC -1- DISEASE: DEFECTS IN PHX ARE THE CAUSE OF REFSUM DISEASE; AN
 CC AUTOSOMAL RECESSIVE DISORDER CHARACTERIZED CLINICALLY BY A TETRAD
 CC OF ABNORMALITIES: RETINITIS PIGMENTOSA, PERIPHERAL NEUROPATHY,
 CC CEREBELLAR ATAXIA, AND ELEVATED PROTEIN LEVELS IN THE
 CC CEREBROSPINAL FLUID (CSF). PATIENTS EXHIBIT ACCUMULATION OF THE
 CC BRANCHED-CHAIN FATTY ACID, PHYANIC ACID, IN BLOOD AND TISSUES.
 CC LESS CONSTANT FEATURES ARE NERVE DEAFNESS, ANOSMIA, SKELETAL
 CC ABNORMALITIES, ICHTHYOSIS, CATARACTS AND CARDIAC IMPAIRMENT.
 CC MANIFESTATIONS OF THE DISEASE APPEAR IN THE SECOND OR THIRD DECADE
 CC OF LIFE.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AF023462; AAB81834.1;
 CC EMBL: AF112977; AAD29632.1;
 CC EMBL: AF242386; AAF74123.1;
 CC EMBL: AF242379; AAF74123.1; JOINED.
 CC EMBL: AF242380; AAF74123.1; JOINED.
 CC EMBL: AF242381; AAF74123.1; JOINED.
 CC EMBL: AF242382; AAF74123.1; JOINED.
 CC EMBL: AF242383; AAF74123.1; JOINED.
 CC EMBL: AF242384; AAF74123.1; JOINED.
 CC EMBL: AF242385; AAF74123.1; JOINED.
 CC Genew: HGNC:8940; PHVH.
 CC MIM: 602026;
 CC MIM: 601996;
 CC MIM: 265500;
 CC Oxidoreductase; Peroxisome; Vitamin C; Iron; Transit peptide;
 KW Disease mutation.
 FT TRANSIT 1 30 MICROBODY (BY SIMILARITY).
 FT CHAIN 31 338 PHYTANOL-COA DIOXYGENASE.
 FT VARIANT 192 192 A -> AA (IN REFSUM).
 FT VARIANT 269 269 /FTID-VAR_012960.
 FT VARIANT 275 275 R > H (IN REFSUM).
 FT VARIANT 275 275 R > W (IN REFSUM; LOSS OF ACTIVITY).
 FT /FTID-VAR_005525.
 FT /FTID-VAR_005526.
 SQ SEQUENCE 338 AA; 38538 MW; FBF9639E7C79A6B0 CRC64;

Query Match 100.0%; Score 28; DB 1; Length 385;
 Best Local Similarity 100.0%; Pred. No. 48;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 1 QDYE 5
 DQ 247 QDYE 241

RESULT 4

SYN_PYPAB STANDARD: PPT: 385 AA
 AC Q9YJ11;
 DI 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE TRYPTOPHANYL-TRNA synthetase (EC 6.1.1.2) (Tryptophan-TRNA ligase)
 GN TPFS OR PAB111.
 OS Pyrococcus abyssi.
 CC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
 CC Pyrococcus.
 CC NCBI_TaxID-29292;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-GE5 / Orsay;
 RA Hellig R.;
 RT "Pyrococcus abyssi genome sequence. Insights into archaeal chromosome
 structure and evolution.";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBI databases
 CC -!- CATALYTIC ACTIVITY: ATP + L-tryptophan + TRNA(trp) -> AMP +
 diphosphate; L-tryptophanyl-TRNA(trp).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
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 or send an email to license@isb-sib.ch).
 CC
 DR EMBL: AJ248288; CAB50601.1;
 DR InterPro: IPR002305; Trp-TRNA-synt_lb.
 DR InterPro: IPR02305; Trp-TRNA-synt_lb.
 DR InterPro: IPR001412; TRNA-synt_1.
 DR Pfam: PF00579; TRNA-synt_lb; 1.
 DR PRINTS: PR01039; TRNASYNTHTRP.
 DR TIGRFAMs: TIGR00233; TPFS; 1.
 DR PROSITE: PS00178; AA-TRNA-LIGASE_1; 1.
 KW Aminoacyl-TRNA synthetase, Protein biosynthesis, Ligase, AIP-binding;
 KW Complete proteome.
 FT SITE 82 90 "HIGH" REGION.
 FT SITE 253 257 "KMSKS" REGION.
 FT SITE 385 AA; 45100 MW; 40200014147412 CP064;
 SQ SEQUENCE 385 AA; 45100 MW; 40200014147412 CP064;

Query Match 100.0%; Score 28; DB 1; Length 385;
 Best Local Similarity 100.0%; Pred. No. 56;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 1 QDYE 5
 DQ 66 QDYE 70

RESULT 5

SYN_CHLPH STANDARD: PPT: 505 AA
 AC Q9J7Z3; Q9JQ14;
 DI 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Glutamyl-TRNA synthetase (EC 6.1.1.17) (Glutamate--TRNA ligase)
 DE (GlutRS).
 CC 551X Gs. J049560.0; Gs-0190.
 OS Chlamydia pneumoniae (Chlamydia pneumoniae).
 CC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydiophila.
 CC NCBI_TaxID-83558;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CWL029;
 RC MEDLINE-99266006; PubMed-10192388;
 RA Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
 RA Olinier L., Grimwood J., Davis R.W., Stephens R.S.;
 RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
 Nat. Genet. 21:385-389(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-AR39;
 RC MEDLINE-20150255; PubMed-10684935;
 RA Read T.D., Brumham K.C., Shen C., Gill S.R., Heidelberg J.F.,
 RA White O., Hickey E.K., Peterson J., Utterback L., Perry K., Bass S.,
 RA Lindler K., Weidman J., Khouri H., Craven H., Bowman C., Dodson R.,
 RA Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
 RA Eisen J., Fraser C.M.;
 RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
 pneumoniae AR39.";
 RL Nucleic Acids Res. 28:1347-1406(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-J138;
 RC MEDLINE-20330349; PubMed-10811462;
 RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Guchi K.,
 RA Shiba T., Ishii K., Hattori M., Kohara S., Nakazawa T.;
 RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
 from Japan and CWL029 from USA.";
 RL Nucleic Acids Res. 28:2311-2314(2000).
 CC -!- CATALYTIC ACTIVITY: ATP + L-glutamate -> TRNA(Glu) -> AMP +
 diphosphate + L-glutamyl-TRNA(Glu).
 CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
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 CC
 DR EMBL: AF001740; A018700.1;
 DR EMBL: AF002140; AAF38063.1;
 DR EMBL: AP002547; HAA98766.1;
 DR HSSP: P27000; 1GLN
 DR TIGR: CP0190;
 DR InterPro: IPR003527; GluX-bact.
 DR InterPro: IPR009224; Glu-TRNA-synt_lb.
 DR InterPro: IPR001412; TRNA-synt_1.
 DR Pfam: PF00749; TRNA-synt_lb; 1.
 DR PRINTS: PR00387; TRNASYNTHGLU.
 DR TIGRFAMs: TIGR00464; GluX-bact; 1.
 DR PROSITE: PS00178; AA-TRNA-LIGASE_1; 1.
 KW Aminoacyl-TRNA synthetase, Protein biosynthesis, Ligase, AIP-binding;
 KW Complete proteome.
 FT SITE 12 22 "HIGH" REGION.
 FT SITE 253 257 "KMSKS" REGION.
 FT BINDING 256 256 ATP (BY SIMILARITY).
 SQ SEQUENCE 505 AA; 58205 MW; 918580D7C31E6695 CP064;

Query Match 100.0%; Score 28; DB 1; Length 505;
 Best Local Similarity 100.0%; Pred. No. 75;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 1 QYEE 5
|||||
DB 54 QYEE 58

RESULT 6
EZRI_BOVIN STANDARD; PRT; 580 AA.
AC P31976;
DT 01-JUL-1993 (Rel. 26, created)
DT 01-JUL-1993 (Rel. 26, last sequence update)
DE 16-OCT-2001 (Rel. 40, last annotation update)
DE Ezrin (p81) (Cyto villin) (Villin 2).
GN VIL2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Artiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN 1
RP SEQUENCE FROM N.A.
RC TISSUE: Brain.
EA Bergson C.M., Zhao H., Salish K., Duman E.S., Nestler E.J.;
RT "Ezrin and osteonectin, two proteins associated with cell shape and
growth, are enriched in the locus coeruleus.";
RL Mol. Cell. Neurosci. 4:64-74(1993).
RN 12
RP SEQUENCE OF 1-15 AND 126-140.
RC TISSUE: Kidney.
EA MEDLINE=96239147; PubMed=8660651;
RA Galat A., Gerbod M.C., Houet F., Riviere S.;
RT "Proteins and their amino acid compositions: uniqueness, variability,
and applications.";
RL Arch. Biochem. Biophys. 330:229-237(1996).
CC 1- FUNCTION: PROBABLY INVOLVED IN CONNECTIONS OF MAJOR CYTOSKELETAL
CC 1- SUBCELLULAR LOCATION: MICROVILLAR PERIPHERAL MEMBRANE PROTEIN
(CYTOPLASMIC SIDE).
CC 1- PTM: PHOSPHORYLATED BY PROTEIN-TYROSINE KINASES.
CC 1- SIMILARITY: CONTAINS 1 BAND 4.1-LIKE DOMAIN.
CC
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CC
EMBL: M98498; AAA30510.1;
InterPro: IPR000290; Band_4.1.
InterPro: IPR000798; Ez/tad/moesin.
Pfam: PF00373; Band_4.1.
Pfam: PF00769; ERM; 1.
PRINTS: PR00935; HAND1.
SMART: SM00295; H41; 1.
PROSITE: PS00660; BAND_4.1.1; 1.
PROSITE: PS00661; BAND_4.1.2; 1.
PROSITE: PS50057; BAND_4.1.3; 1.
KW Structural protein; Cytoskeleton; Phosphorylation.
FI INI_MET 0 0
FI DOMAIN 57 224 BAND 4.1-LIKE.
FI MOD_RES 145 145 PHOSPHORYLATION (BY PDGFR)
ET MOD_RES 353 353 (BY SIMILARITY).
ET MOD_RES 353 353 PHOSPHORYLATION (BY PDGFR)
SU SEQUENCE 580 AA; 68629 MW; MCD663E5C200FAA3 CRC64;
Query Match 100.0%; Score 28; DB 1; Length 580;
Best Local Similarity 100.0%; Pred No. 88;
Matches %; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYEE 5

DB 351 QYEE 355
|||||

RESULT 7
EZRI_HUMAN STANDARD; PRT; 585 AA.
AC P15311; P23714; Q9NSJ4;
DT 01-APR-1990 (Rel. 14, created)
DT 01-NOV-1991 (Rel. 20, last sequence update)
DT 15-JUN-2002 (Rel. 41, last annotation update)
DE Ezrin (p81) (Cyto villin) (Villin 2).
GN VIL2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 1
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC MEDLINE=90076135; PubMed=2591371;
EA Gould K.L., Bretscher A., Esch F.S., Hunter T.;
RT "cDNA cloning and sequencing of the protein tyrosine kinase
substrate, ezrin, reveals homology to band 4.1.";
RL EMBO J. 8:4133-4142(1989).
RN 12
RP SEQUENCE FROM N.A.
RC TISSUE-Placenta;
EA MEDLINE=89380299; PubMed=2674140;
RA Turunen O., Winqvist R., Pakkanen R., Grzeschik K.H., Wahlstrom T.,
RA Vaheri A.;
RT "Cyto villin, a microvillar Mr 75,000 protein, cDNA sequence,
prokaryotic expression, and chromosomal localization.";
RL J. Biol. Chem. 264:16727-16732(1989).
RN 13
RP SEQUENCE FROM N.A.
RC Ottenwälder H., Obermaier B., Mewes H.-W., Weill R., Wiemann S.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN 14
RP SEQUENCE OF 171-179 AND 342-349.
EA MEDLINE=96311348; PubMed=8713105;
RA Egerlon M., Moritz R.L., Drucker B., Kelso A., Simpson R.J.;
RT "Identification of the 70kD heat shock cognate protein (hsc70) and
alpha-actinin-1 as novel phosphotyrosine-containing proteins in T
lymphocytes.";
RL Biochem. Biophys. Res. Commun. 224:666-674(1996).
RN 15
RP PHOSPHORYLATION BY PDGFR.
EA MEDLINE=92406858; PubMed=1382070;
RA Krieg J., Hunter T.;
RT "Identification of the two major epidermal growth factor-induced
tyrosine phosphorylation sites in the microvillar core protein
ezrin.";
RL J. Biol. Chem. 267:19258-19266(1992).
RN 16
RP PHOSPHORYLATION.
EA MEDLINE=92388649; PubMed=1381389;
RA Egerlon M., Burqess W.H., Chen D., Drucker B.J., Bretscher A.,
RA Samelson L.E.;
RT "Identification of ezrin as an 81 kDa tyrosine phosphorylated protein
in T cells.";
RL J. Immunol. 149:1847-1852(1992).
CC 1- FUNCTION: PROBABLY INVOLVED IN CONNECTIONS OF MAJOR CYTOSKELETAL
CC STRUCTURES TO THE PLASMA MEMBRANE.
CC 1- SUBCELLULAR LOCATION: MICROVILLAR PERIPHERAL MEMBRANE PROTEIN
CC (CYTOPLASMIC SIDE).
CC 1- TISSUE SPECIFICITY: COMPONENT OF THE MICROVILLI OF INTESTINAL
CC EPITHELIAL CELLS.
CC 1- PTM: PHOSPHORYLATED BY PROTEIN-TYROSINE KINASES.
CC 1- SIMILARITY: CONTAINS 1 BAND 4.1-LIKE DOMAIN.
CC
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EMBL: X51521; CAA35893.1; ...
EMBL: J95021; AAG62278.1; ALT_INIT.
EMBL: AL162086; CAB92418.1; ALT_INIT.
PIR: S09263; S09263.
PIR: A34400; A34400.
SWISS-2DPAGE: P15311; HUMAN.
Genbank: U00126.1; V112
MIM: 123900;

InterPro: IPR000299; Rand_4.1
Pfam: PF00373; Rand_4.1; 1.
Pfam: PF00769; KRM; 1.
PRINTS: P500935; BAND41.
SMART: SM00295; B41; 1.
PROSITE: PS00660; BAND_41_1; 1.
PROSITE: PS00661; BAND_41_2; 1.
PROSITE: PS00557; BAND_41_3; 1.
KW Structural protein; Cytoskeleton; Phosphorylation.

INIT_MET 0
DOMAIN 57 224 BAND 4.1-LIKE
MOD_RES 145 145 PHOSPHORYLATION (BY PGFR).
MOD_RES 353 353 PHOSPHORYLATION (BY PGFR).
CONFLICT 531 531 V -> L (IN REF. 3).
SEQUENCE 585 AA: 69267 MW: 268440; 406380; 22 Cys54;

Query Match 100.0%; Score 28; DB 1; Length 585;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDYE 5
Db 351 QDYE 355

RESULT 8
ID DSK1_CYLFU STANDARD: PPT: 624 AA
AC Q39493;
DT 01-NOV-1997 (Rel. 35, Created)
DI 01-NOV-1997 (Rel. 35, Last sequence update)
DE DSK1, a novel kinesin-related protein from the diatom *Cylindrotheca fusiformis* that is involved in anaphase spindle elongation.
GN DSK1.
OS *Cylindrotheca fusiformis* (Marine diatom)
OC Eukaryota; Stramenopiles; Bacillariophyta; Bacillariophyceae;
OC Bacillariophyceae; Bacillariales; Bacillariaceae; Cylindrothecae;
OX NCBI_TaxID: 2853;
RN [1]
RP SEQUENCE FROM N A
PX MEDLINE: 96222363; PubMed: 8636234.
PT DSK1, a novel kinesin-related protein from the diatom *Cylindrotheca fusiformis* that is involved in anaphase spindle elongation.
RT J. Cell Biol. 133:595-604(1996).
RL FUNCTION: INVOLVED IN ANAPHASE SPINDLE ELONGATION.
CC -!- FUNCTION: INVOLVED IN ANAPHASE SPINDLE ELONGATION.
CC -!- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY MCAK/KIP2 SUBFAMILY

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PMR: 051680; AAR05681.1;
HSP: P17119; 3KAR.

InterPro: IPR001772; Kinesin_motor.
Pfam: PF00225; Kinesin; 1.
PRINTS: P00380; KINESINHEAVY.
SMART: SM00129; KISC; 1.
PROSITE: PS00411; KINESIN_MOTOR_DOMAIN; 1.
PROSITE: PS00667; KINESIN_MOTOR_DOMAIN; 1.
KW Motor protein; Microtubules; ATP binding; Coiled coil.
FT DOMAIN 1 85 GLOBULAR (POTENTIAL).
FT DOMAIN 86 425 KINESIN-MOTOR (BY SIMILARITY).
FT NP_BIND 426 624 COILED COIL (POTENTIAL).
FT NP_BIND 186 193 ATP (POTENTIAL).
SQ SEQUENCE 624 AA: 75368 MW: 69968; 122262; 155 Cys44;

Query Match 100.0%; Score 28; DB 1; Length 624;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDYE 5
Db 505 QDYE 509

RESULT 9
ID SYQ_SCHPO STANDARD: PPT: 811 AA.
AC Q9VY8;
DI 16-OCT-2001 (Rel. 40, Created)
DI 16-OCT-2001 (Rel. 40, Last sequence update)
DI 16-JUN-2002 (Rel. 41, Last annotation update)
DE Probable glutamyl-tRNA synthetase (EC 6.1.1.18) (Glutamine-tRNA ligase) (GlnRS).
GN SPB342.02.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetes; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID: 4896;
RN [1]
RP SEQUENCE FROM N.A.

STRAIN: 972;
MEDLINE: 21848401; PubMed: 11859360;
Pfam: P00111; Gwiliam P., Rajadurai M.A., Lyne M., Lyne P., Stewart A., Squares J., Peal N., Hayles J., Baker S., Basham D., Bowman S., Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A., Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Holliday S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., James K., Jones L., Jones M., Leather S., McDonald S., McLean J., McNeely P., Moule S., Murtagh K., Murphy I., Niblett D., Odell C., Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E., Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S., Skilton J., Simmonds M., Squares R., Squares S., Stevens K., Taylor K., Taylor K.G., Tivey A., Walsh S.V., Watling L., Whitehead S., Woodward T., Vekic G., Aert P., Pothof T., Gryncper B., Welljous I., Vansteenkiste E., Kieger M., Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Felle C., Holzer E., Moestl D., Hilbert H., Berrym K., Langer T., Beck A., Lichtner H., Reinhardt K., Pohl T.M., Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B., Goffeau A., Cadieu E., Drgano S., Gloux S., Leleau V., Mottier S., Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Lucas M., Peche M., Gaillardin C., Tallada V.A., Garde A., Thode G., Pava P., Cruzado L., Timoney T., Sanchez M., del Rey F., Benito J., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S., Cetrulli L., Lowe T., McCumbie W.P., Paulsen O., Nurse P., Shpakovski G.V., Ussery D., Harteil H.G., Nurse P., Nature 415:871-889(2002).
CC -!- CATALYTIC ACTIVITY: ATP + L-glutamine + tRNA(Gln) = AMP + diphosphate + L-glutamyl-tRNA(Gln).
CC -!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.

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ID D620_MOUSE STANDARD: PRT: 825 AA.
 AC Q9JY4: Q9JY4; (rel. 40, created)
 DT 16-OCT-2001 (rel. 40, last sequence update)
 DI 16-OCT-2001 (rel. 40, last annotation update)
 DE Probable ATP-dependent PNA helicase DDX20 (DEAD-box protein 20) (DEAD-box protein DP103) (Component of gems 3) (Gemin3) (Regulator of steroidogenic factor-1) (ROSF-1)
 DE Steroidogenic factor-1 (ROSF-1)
 GN DDX20 OR GEMIN3 OR DP103.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20231537; PubMed=10767334;
 RA Campbell L., Hunter K.M., Molaghegh P., Tinsley J.M., Brasch M.A., Davies K.E.;
 RT "Direct interaction of Smn with dp103, a putative RNA helicase: a role for Smn in transcription regulation?";
 RT Hum. Mol. Genet. 9:1093-1100(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/c; TISSUE-Testis;
 PA "Q. Mueller, I.F. Berg, G. Yao X., Crawford P.A., Sadeisky Y.;
 RT "The DEAD box protein DDX20 is a regulator of steroidogenic factor-1";
 RT J. Biol. Chem. 275:1093-1100(2000).
 RN [3]
 RP Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases
 RC -!- FUNCTION: THE SMN COMPLEX PLAYS AN ESSENTIAL ROLE IN SPLICEOSOMAL SNRP ASSEMBLY IN THE CYTOPLASM, AND IS REQUIRED FOR PPE-MPNA SPLICING IN THE NUCLEUS.
 CC -!- SUBUNIT: FORMS A STABLE HETEROMERIC COMPLEX WITH SURVIVAL OF MOTOR NEURON PROTEIN (SMN), GEMIN2 AND GEMIN3. INTERACTS DIRECTLY WITH SMN, SM B, SM D2 AND SM D3.
 CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC AND NUCLEAR. LOCALIZED IN SUBNUCLEAR STRUCTURES NEXT TO SPLENDID BODIES, CALLED GEMS, WHICH ARE HIGHLY ENRICHED IN SPLICEOSOMAL SNRNPs.
 CC -!- SIMILARITY: BELONGS TO THE DEAD BOX HELICASE FAMILY.
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 CC
 DR EMBL: AJ250027; CAB86201.1;
 DR EMBL: AF220454; AAF76381.1;
 DR HSSP: Q580A3; 1HV8
 DR MGI: 1658415; DDX20.
 DR InterPro: IPR001410; DEAD.
 DR InterPro: IPR000429; DEAD_BOX.
 DR InterPro: IPR001850; Helicase_C.
 DR Pfam: PF00270; DEAD; 1.
 DR Pfam: PF00271; Helicase_C; 1.
 DR SMART: SM00487; DDXC; 1.
 DR SMART: SM00490; HELICC; 1.
 DR SMART: SF00049; DEAD-ATP-HELICASE; 1.
 KW Helicase. ATP-binding, DNA-binding; Nuclear protein; mRNA processing.
 FT NP_BIND 107 114 ATP (POTENTIAL).
 FT SITE 212 215 DEAD BOX.
 FT CONFLICT 5 5 A -> T (IN REF. 2).
 FT CONFLICT 9 9 P -> R (IN REF. 2).
 FT CONFLICT 226 226 E -> G (IN REF. 2).
 FT CONFLICT 468 468 V -> I (IN REF. 2).
 SQ SEQUENCE 825 AA; 91719 MW; F6D06E2EA87A7D2D CRC64;

Query Match 100.0% Score 28, DR 1, Length 825,

Best Local Similarity 100.0%, Prod. No. 13032,

Matches 5; Conservativeness 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDYE 5
 DB 772 QDYE 776
 RESULT 12
 IKAP_HUMAN
 ID IKAP_HUMAN STANDARD: PRT: 1332 AA.
 AC Q9J163; Q9J163; Q9J163;
 DT 16-OCT-2001 (rel. 40, created)
 DI 16-OCT-2001 (rel. 40, last sequence update)
 DE Probable ATP-dependent PNA helicase DDX20 (DEAD-box protein 20) (DEAD-box protein DP103) (Component of gems 3) (Gemin3) (Regulator of steroidogenic factor-1) (ROSF-1)
 DE Steroidogenic factor-1 (ROSF-1)
 GN DDX20 OR GEMIN3 OR DP103.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.; AND PARTIAL SEQUENCE.
 RC TISSUE=Cervical carcinoma;
 RA Cohen L., Hensel W.J., Baeuerle P.A.;
 RT "IFAF is a scaffolding protein of the IkappaB kinase complex";
 RT Nature 395:292-296(1998).
 RN [2]
 RP SEQUENCE FROM N.A.; AND VARIANT PD PRO-696.
 RX MEDLINE=2109531; PubMed=11179008;
 PA Slagter M.P., Liebert C.B., Chadwick B.P., Idelson M., Reznik L., Rodriguez C.M., Makalowska I., Brownstein M.J., Krappmann D., Scheiderer C., Maayan C., Axelrod P.B., Guseilla J.P.;
 RT "Tissue specific expression of a splicing mutation in the IKKAP gene causes familial dysautonomia";
 RT Am. J. Hum. Genet. 68:598-605(2001).
 RN [3]
 RP SEQUENCE OF 961-1332 FROM N.A.
 RC TISSUE=Brain;
 RA Wambutt R., Houbert R., Mowes H.W., Gassenhuber J., Wichmann S.;
 RT Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP VARIANT PD PRO-696, AND EFFECT ON PHOSPHORYLATION.
 RX MEDLINE=2109044; PubMed=11179021;
 RA Anderson S., Coll F., Daly L.W., Kichula E.A., Rork M.J., Volpi S.A., Ekstein J., Rubin B.Y.;
 RT "Familial dysautonomia is caused by mutations of the IKAP gene";
 RT Am. J. Hum. Genet. 68:753-758(2001).
 CC -!- FUNCTION: MAY ACT AS A SCAFFOLD PROTEIN THAT MAY ASSEMBLE ACTIVE IKK-MAP3K14 COMPLEXES (IKKA, IKKB AND MAP3K14/NIK).
 CC -!- SUBUNIT: INTERACTS PREFERENTIALLY WITH MAP3K14/NIK FOLLOWED BY IKK-ALPHA AND IKK-BETA.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- PTM: PHOSPHORYLATED.
 CC -!- DISEASE: DEFECTS IN IKKAP ARE THE CAUSE OF FAMILIAL DYSAUTONOMIA (FD). ALSO KNOWN AS RILEY-DAY SYNDROME OR HEREDITARY SENSORY AND AUTONOMIC NEUROPATHY TYPE III. THIS AUTOSOMAL RECESSIVE DISORDER IS DUE TO THE POOR DEVELOPMENT AND SURVIVAL, AND PROGRESSIVE DEGENERATION OF THE SENSORY, SYMPATHETIC AND PARASYMPATHETIC NERVE FIBERS. PD INDIVIDUALS ARE AFFECTED WITH A VARIETY OF SYMPTOMS SUCH AS DECREASED SENSITIVITY TO PAIN AND TEMPERATURE, CARDIOVASCULAR INSTABILITY, RECURRENT PNEUMONIAS, VOMITING CRISES, AND GAS-INDUCED BRONCHOSPASM. IT IS PRIMARILY CONFINED TO INDIVIDUALS OF ASHKENAZI JEWISH DESCENT, WITH AN INCIDENCE OF 1/4600 LIVE BIRTHS.
 CC -!- CAUTION: REF. 3 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A FRAMESHIFT IN POSITION 1286.
 CC
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Dh 56 QDYEQ 60
1111:

RESULTS

Query Match	Best Match	Matches	4; Conservative	1; Mismatches	0; Idents	0; Gaps
89.4%	Score 25;	DB 1;	Length 134;			
80.0%	Pre. No. 79;					
4;	Conservative	1;	Mismatches	0;	Idents	0;

Search completed: January 16, 2003, 16:51:17
Job time : 8.28571 secs

